FILE 'STNGUIDE' ENTERED AT 11:26:17 ON 02 FEB 2005

FILE 'MEDLINE, BIOSIS, CAPLUS, AGRICOLA, ESBIOBASE, AQUASCI' ENTERED AT 11:27:31 ON 02 FEB 2005
D 100, 107 110, 97 BIB AB

FILE 'STNGUIDE' ENTERED AT 11:27:32 ON 02 FEB 2005

FILE 'MEDLINE, BIOSIS, CAPLUS, AGRICOLA, ESBIOBASE, AQUASCI' ENTERED AT 11:32:39 ON 02 FEB 2005
D 65 103 2 29 40 54 BIB AB

FILE 'STNGUIDE' ENTERED AT 11:32:41 ON 02 FEB 2005

INDEX '1MOBILITY, 2MOBILITY, ABI-INFORM, ADISCTI, AEROSPACE, AGRICOLA, ALUMINIUM, ANABSTR, ANTE, APOLLIT, AQUALINE, AQUASCI, AQUIRE, BABS, BIBLIODATA, BIOBUSINESS, BIOCOMMERCE, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, BLLDB, CABA, CANCERLIT, ...' ENTERED AT 11:41:47 ON 02 FEB 2005
SEA (INTRAOPERATIVE OR OPERAT? OR SURGER? OR BIOPS?) AND (PCR O

3	FILE 1MOBILITY
144	FILE ABI-INFORM
300	FILE ADISCTI
11	FILE AEROSPACE
152	FILE AGRICOLA
59	FILE ANABSTR
6	FILE ANTE
2	FILE APOLLIT
26	FILE AQUALINE
76	FILE AQUASCI
41	FILE BABS
2	FILE BIBLIODATA
27	FILE BIOBUSINESS
12	FILE BIOCOMMERCE
396	FILE BIOENG
11628	FILE BIOSIS
1355	FILE BIOTECHABS
1355	FILE BIOTECHDS
10806	FILE BIOTECHNO
1114	FILE CABA
6427	FILE CANCERLIT
7076	FILE CAPLUS
87	FILE CBNB
49	FILE CEABA-VTB
63	FILE CEN
1	FILE CERAB
26	FILE CIN
8	FILE CIVILENG
207	FILE COMPENDEX
5	FILE COMPUAB
1	FILE COMPUSCIENCE
27	FILE CONFSCI
3	FILE COPPERLIT
5	FILE CROPU
4	FILE CSNB
184	FILE DDFU
11113	FILE DGENE
255	FILE DISSABS
6	FILE DPCI
925	FILE DRUGU
7	FILE ELCOM

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    1   FILE EMA
  200   FILE EMBAL
16011   FILE EMBASE
   39   FILE ENCOMPLIT
   18   FILE ENCOMPPAT
  163   FILE ENERGY
   16   FILE ENTEC
   32   FILE ENVIROENG
  183   FILE EPFULL
 6071   FILE ESBIOBASE
    1   FILE FORIS
    2   FILE FRANCEPAT
  808   FILE FRFULL
   30   FILE FROSTI
   55   FILE FSTA
  337   FILE GENBANK
   18   FILE HEALSAFE
    1   FILE ICONDA
 1629   FILE IFIPAT
    3   FILE IMSDRUGNEWS
   93   FILE INIS
  122   FILE INPADOC
  110   FILE INSPEC
    5   FILE INSPHYS
 2489   FILE INVESTEXT
   38   FILE IPA
    5   FILE ITRD
  115   FILE JAPIO
 5522   FILE JICST-EPLUS
   19   FILE KOREAPAT
   29   FILE KOSMET
 2400   FILE LIFESCI
    2   FILE MATBUS
    2   FILE MATH
    4   FILE MECHENG
15372   FILE MEDLINE
   37   FILE METADEX
   11   FILE NIOSHTIC
 1549   FILE NLDB
   54   FILE NTIS
   31   FILE OCEAN
    4   FILE PAPERCHEM2
 8386   FILE PASCAL
    4   FILE PATDPA
 1795   FILE PATDPAFULL
49340   FILE PCTFULL
    8   FILE PHARMAML
    2   FILE PHIC
  188   FILE PHIN
   10   FILE PIRA
   26   FILE POLLUAB
 2117   FILE PROMT
    7   FILE RAPRA
11729   FILE SCISEARCH
    4   FILE SOLIDSTATE
  104   FILE TEMA
    1   FILE TEXTILETECH
 3896   FILE TOXCENTER
    7   FILE TULSA
   11   FILE UFORDAT
   20   FILE ULIDAT
46151   FILE USPATFULL
 3119   FILE USPAT2
```

ACCESSION NUMBER: 2004:33869 BIOSIS
DOCUMENT NUMBER: PREV200400031975
TITLE: HELICOBACTER PYLORI-MEDIATED REGULATION OF INTERLEUKIN-8 (IL-8) TRANSCRIPTION IN GASTRIC EPITHELIAL CELLS: ROLE OF APURINIC/APYRIMIDINIC ENDONUCLEASE-1/REDOX FACTOR-1 (APE-1/REF-1). .
AUTHOR(S): O'Hara, Ann [Reprint Author]; Ding, Song-Ze; Ryan, Kieran; Mitra, Sankar; Izumi, Tadahito; Mifflin, Randy; Crowe, Sheila E.
CORPORATE SOURCE: Charlottesville, VA, USA
SOURCE: Digestive Disease Week Abstracts and Itinerary Planner, (2003) Vol. 2003, pp. Abstract No. 353. e-file.
Meeting Info.: Digestive Disease 2003. FL, Orlando, USA. May 17-22, 2003. American Association for the Study of Liver Diseases; American Gastroenterological Association; American Society for Gastrointestinal Endoscopy; Society for Surgery of the Alimentary Tract.
DOCUMENT TYPE: Conference; (Meeting)
Conference; (Meeting Poster)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 7 Jan 2004
Last Updated on STN: 7 Jan 2004

AB Background:We have previously shown that Helicobacter pylori infection increases expression of IL-8 and apurinic/apyrimidinic endonuclease-1/redox factor-1 (APE-1/Ref-1) in human gastric epithelial cells. APE-1/Ref-1 repairs oxidatively damaged DNA and reductively activates transcription factors including the activator protein (AP)-1 complex (c-Jun/c-Fos) and NF-kappaB. The aim of this study was to examine whether APE-1/Ref-1 modulates IL-8 gene expression in H. pylori-infected gastric epithelial cells. Methods: H. pylori (Hp) 26695 or the cag PAI deficient isogenic mutant, 8-1, for varying times. IL-8 was measured in cell supernatants by ELISA and EMSAs were used to examine AP-1 and NF-kappaB binding in nuclear extracts. APE-1/Ref-1 expression was assayed by western blot and by real-time RT-PCR (**Cepheid Smart Cycler**). The effect of APE-1/Ref-1 overexpression was assessed in AGS cells transfected with an APE-1/Ref-1 expression vector and co-transfected with a luciferase-linked IL-8 reporter construct containing AP-1 and NF-kappaB binding sites (-1498/+44 IL-8 luc). Results: Both strains of H. pylori increased APE-1/Ref-1 protein and mRNA expression but only the cag PAI bearing strain induced IL-8 secretion. Compared to other stimuli, Hp 26695 had the greatest and most rapid effect on AP-1 and NF-kappaB binding. Enhanced IL-8 transcription was detected in cells that overexpressed APE-1/Ref-1 compared to cells with basal levels of APE-1/Ref-1. Hp 26695 induced higher levels of IL-8 transcription compared to uninfected controls and this difference was further increased in cells overexpressing APE-1/Ref-1. Overexpression of APE-1/Ref-1 was confirmed by western blot and real-time PCR. Conclusion: These results indicate that APE-1/Ref-1, which is increased in response to H. pylori infection and oxidative stress, plays a role in the transactivation of IL-8 transcription. Our findings suggest that H. pylori induced transcription factor binding activity is mediated by APE-1/Ref-1 and together, these data further implicate APE-1/Ref-1 as playing a pivotal role in regulating the epithelial response to H. pylori infection.
Supported by RO1 DK61769-01..

L1 ANSWER 7 OF 16 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN
ACCESSION NUMBER: 2003:545152 BIOSIS
DOCUMENT NUMBER: PREV200300546468
TITLE: Detection and quantification of total and potentially virulent Vibrio parahaemolyticus using a 4-channel multiplex real-time PCR targeting the tl, tdh, and trh genes and a novel PCR internal control.

AUTHOR(S): Vickery, M. C. L. [Reprint Author]; Blackstone, G. M. [Reprint Author]; Nordstrom, J. L. [Reprint Author]; Depaola, A. [Reprint Author]
CORPORATE SOURCE: Gulf Coast Seafood Laboratory, U.S. FDA, Dauphin Island, AL, USA
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (2003) Vol. 103, pp. Q-082. http://www.asmusa.org/mtgsrc/generalmeeting.htm. cd-rom. Meeting Info.: 103rd American Society for Microbiology General Meeting. Washington, DC, USA. May 18-22, 2003. American Society for Microbiology. ISSN: 1060-2011 (ISSN print).
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 19 Nov 2003
Last Updated on STN: 19 Nov 2003
AB Vibrio parahaemolyticus (Vp) is an estuarine bacterium that is the leading cause of shellfish-associated cases of bacterial gastroenteritis in the U.S.. The thermolabile hemolysin gene (tl) is a species-specific marker for V. p.; the thermostable direct hemolysin gene (tdh) and t

Using molecular beacons to detect single-nucleotide polymorphisms with real-time PCR.
AUTHOR: Mhlanga M.M.; Malmberg L.
CORPORATE SOURCE: L. Malmberg, Department of Medical Sciences, Molecular Medicine, Uppsala University Hospital, S-75185-Uppsala, Sweden. loma0102@student.uu.se
SOURCE: Methods, (2001) 25/4 (463-471).
Refs: 22
ISSN: 1046-2023 CODEN: MTHDE
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 027 Biophysics, Bioengineering and Medical Instrumentation
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Detection of single-nucleotide polymorphisms (SNPs) in high-throughput studies promises to be an expanding field of molecular medicine in the near future. Highly specific, simple, and accessible methods are needed to meet the rigorous requirements of single-nucleotide detection needed in pharmacogenomic studies, linkage analysis, and the detection of pathogens. Molecular beacons present such a solution for the high-throughput screening of SNPs in homogenous assays using the polymerase chain reaction (PCR). Molecular beacons are probes that fluoresce on hybridization to their perfectly complementary targets. In recent years they have emerged as a leading genetic analysis tool in a wide range of contexts from quantification of RNA transcripts, to probes on microarrays, to single-nucleotide polymorphism detection. The majority of these methods use PCR to obtain sufficient amounts of sample to analyze. The use of molecular beacons with other amplification schemes has been reliably demonstrated, though PCR remains the method of choice. Here we discuss and present how to design and use molecular beacons to achieve reliable SNP genotyping and allele discrimination in real-time PCR. In addition, we provide a new means of analyzing data outputs from such real-time PCR assays that compensates for differences between sample condition, assay conditions, variations in fluorescent signal, and amplification efficiency. The mechanisms by which molecular beacons are able to have extraordinary specificity are also presented. .COPYRGT. 2001 Elsevier Science (USA).

L1 ANSWER 5 OF 16 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN
ACCESSION NUMBER: 2004:259874 BIOSIS
DOCUMENT NUMBER: PREV200400258737
TITLE: Improving the accuracy of genetic diagnosis from single cells through analysis of real-time PCR signal kinetics.
AUTHOR(S): Pierce, Kenneth E. [Reprint Author]; Rice, John E. [Reprint Author]; Sanchez, Aquiles [Reprint Author]; Wangh, Lawrence J. [Reprint Author]
CORPORATE SOURCE: Brandeis Univ, Waltham, MA, USA
SOURCE: Fertility and Sterility, (September 2003) Vol. 80, No. Suppl. 3, pp. S9. print.
Meeting Info.: 59th Annual Meeting of the American Society for Reproductive Medicine. San Antonio, Texas, USA. October 11-15, 2003. American Society for Reproductive Medicine.
ISSN: 0015-0282 (ISSN print).
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 19 May 2004
Last Updated on STN: 19 May 2004

L1 ANSWER 6 OF 16 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN

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            23   FILE VETU
            30   FILE WATER
             1   FILE WELDASEARCH
          1062   FILE WPIDS
             3   FILE WPIFV
          1062   FILE WPINDEX
             3   FILE WSCA
L5              QUE (INTRAOPERATIVE OR OPERAT? OR SURGER? OR BIOPS?) AND (PCR
                OR POLYMERASE (W) CHAIN)
                ---------
                D RANK

     FILE 'EMBASE, MEDLINE, SCISEARCH, BIOSIS, BIOTECHNO, PASCAL, CAPLUS,
     CANCERLIT, ESBIOBASE, JICST-EPLUS, TOXCENTER, USPAT2, LIFESCI, PROMT,
     PATDPAFULL, IFIPAT, NLDB, BIOTECHDS, CABA, WPIDS, DRUGU, FRFULL, BIOENG,
     GENBANK, ADISCTI, DISSABS, COMPENDEX, ...' ENTERED AT 11:49:25 ON 02 FEB
     2005
L6         26928 SEA (INTRAOPERATIVE OR OPERAT? OR SURGER? OR BIOPS?) (14A)
                 (PCR OR POLYMERASE (W) CHAIN)
L7           758 SEA L6 AND (ULTRAFAST OR RAPID OR FAST OR QUICK) (4A) (PCR OR
                 POLYMERASE (W) CHAIN)
L8           211 SEA L6 AND INTRAOPERATIVE
L9            73 DUP REM L8 (138 DUPLICATES REMOVED)
                 D 1-73 TI
                 D 71 BIB AB
                 D 69 BIB AB
L10          381 SEA L6 AND (DURING (3A) SURGERY)
L11           89 DUP REM L10 (292 DUPLICATES REMOVED)
                 D 1-89 TI
                 D 38 53 BIB AB
L12           46 SEA L7 AND (INTRAOPERATIVE OR DURING (3A) SURGERY)
L13           14 DUP REM L12 (32 DUPLICATES REMOVED)
                 D 1-14 TI
                 D 10-14 BIB AB


     FILE HOME

     FILE MEDLINE
      FILE LAST UPDATED: 29 JAN 2005 (20050129/UP).  FILE COVERS 1950 TO DATE.

      On December 19, 2004, the 2005 MeSH terms were loaded.

      Warning: The search L-number/HUMAN limit is missing from records indexed
      with the new 2005 MeSH (records added since December 19, 2004).  Until
      this is corrected, include HUMANS/CT and 20041219-20051231/ED in
      searches to limit results to humans for this time period.

      OLDMEDLINE now back to 1950.

      MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
      MeSH 2005 vocabulary.  See http://www.nlm.nih.gov/mesh/ and
      http://www.nlm.nih.gov/pubs/techbull/nd03/nd03_mesh.html for a
      description of changes.

      This file contains CAS Registry Numbers for easy and accurate
      substance identification.

     FILE BIOSIS
     FILE COVERS 1969 TO DATE.
     CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
     FROM JANUARY 1969 TO DATE.
```

RECORDS LAST ADDED: 26 January 2005 (20050126/ED)

FILE RELOADED: 19 October 2003.

FILE CAPLUS

FILE COVERS 1907 - 2 Feb 2005 VOL 142 ISS 6
FILE LAST UPDATED: 1 Feb 2005 (20050201/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE AGRICOLA

FILE COVERS 1970 TO 10 Jan 2005 (20050110/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE ESBIOBASE
FILE LAST UPDATED: 1 FEB 2005 <20050201/UP>
FILE COVERS 1994 TO DATE.

>>> SIMULTANEOUS LEFT AND RIGHT TRUNCATION AVAILABLE IN /CC, /ORGN, AND /ST <<<

FILE JICST-EPLUS
FILE COVERS 1985 TO 24 JAN 2005 (20050124/ED)

THE JICST-EPLUS FILE HAS BEEN RELOADED TO REFLECT THE 1999 CONTROLLED TERM (/CT) THESAURUS RELOAD.

FILE AQUASCI
FILE COVERS 1978 TO 19 Jan 2005 (20050119/ED)

FILE STNGUIDE
FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Jan 28, 2005 (20050128/UP).

FILE STNINDEX

FILE EMBASE
FILE COVERS 1974 TO 27 Jan 2005 (20050127/ED)

EMBASE has been reloaded. Enter HELP RLOAD for details.

This file contains CAS Registry Numbers for easy and accurate

substance identification.

FILE SCISEARCH
FILE COVERS 1974 TO 27 Jan 2005 (20050127/ED)

FILE BIOTECHNO
FILE LAST UPDATED: 7 JAN 2004 <20040107/UP>
FILE COVERS 1980 TO 2003.

>>> BIOTECHNO IS NO LONGER BEING UPDATED AS OF 2004 <<<

>>> SIMULTANEOUS LEFT AND RIGHT TRUNCATION AVAILABLE IN /CT AND BASIC INDEX <<<

FILE PASCAL
FILE LAST UPDATED: 31 JAN 2005 <20050131/UP>
FILE COVERS 1977 TO DATE.

>>> SIMULTANEOUS LEFT AND RIGHT TRUNCATION IS AVAILABLE IN THE BASIC INDEX (/BI) FIELD <<<

FILE CANCERLIT
FILE COVERS 1963 TO 15 Nov 2002 (20021115/ED)

On July 28, 2002, CANCERLIT was reloaded. See HELP RLOAD for details.

CANCERLIT thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2002 vocabulary. Enter HELP THESAURUS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE TOXCENTER

FILE COVERS 1907 TO 1 Feb 2005 (20050201/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

TOXCENTER has been enhanced with new files segments and search fields. See HELP CONTENT for more information.

TOXCENTER thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2005 vocabulary. See http://www.nlm.nih.gov/mesh/ and http://www.nlm.nih.gov/pubs/techbull/nd03/nd03_mesh.html for a description of changes.

FILE USPAT2

FILE COVERS 2001 TO PUBLICATION DATE: 1 Feb 2005 (20050201/PD)
FILE LAST UPDATED: 1 Feb 2005 (20050201/ED)
HIGHEST GRANTED PATENT NUMBER: US2004230467
HIGHEST APPLICATION PUBLICATION NUMBER: US2005021284
CA INDEXING IS CURRENT THROUGH 1 Feb 2005 (20050201/UPCA)
ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 1 Feb 2005 (20050201/PD)
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Dec 2004
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Dec 2004

USPAT2 is a companion file to USPATFULL. USPAT2 contains full text of the latest US publications, starting in 2001, for the inventions covered in USPATFULL. USPATFULL contains full text of the original published US patents from 1971 to date and the original applications from 2001. In addition, a USPATFULL record for an invention contains

a complete list of publications that may be searched in standard search fields, e.g., /PN, /PK, etc.

USPATFULL and USPAT2 can be accessed and searched together through the new cluster USPATALL. Type FILE USPATALL to enter this cluster.

Use USPATALL when searching terms such as patent assignees, classifications, or claims, that may potentially change from the earliest to the latest publication.

FILE LIFESCI
FILE COVERS 1978 TO 14 Jan 2005 (20050114/ED)

FILE PROMT
FILE COVERS 1978 TO 2 FEB 2005 (20050202/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE PATDPAFULL
FILE LAST UPDATED: 27 JAN 2005 <20050127/UP>
MOST RECENT UPDATE WEEK: 200504 <200504/EW>
FILE COVERS 1987 TO DATE

<<< PATDPAFULL HAS BEEN UPDATED.
HOWEVER, SOME BIBLIOGRAPHIC FIELDS ARE STILL MISSING.
---> SEE 'HELP CHANGE'.
THESE FIELDS WILL BE LOADED SOON. >>>

<<< PATDPAFULL WURDE FORTGESCHRIEBEN.
ALLERDINGS FEHLEN NOCH EINIGE BIBLIOGRAFISCHE FELDER.
---> SIEHE 'HELP CHANGE'.
DIESE WERDEN IN KUERZE NACHGELADEN. >>>

FILE IFIPAT
FILE COVERS 1950 TO PATENT PUBLICATION DATE: 1 Feb 2005 (20050201/PD)
FILE LAST UPDATED: 1 Feb 2005 (20050201/ED)
HIGHEST GRANTED PATENT NUMBER: US2005004268
HIGHEST APPLICATION PUBLICATION NUMBER: US2005022281
UNITERM INDEXING IS AVAILABLE IN THE IFIUDB FILE
UNITERM INDEXING LAST UPDATED: 31 Jan 2005 (20050131/UP)
INDEXING CURRENT THROUGH PAT PUB DATE: 27 Nov 2003 (20031127/PD)

INCL, INCLM, INCLS fields added. Please refer to ONLINE News for details.

FILE NLDB
FILE COVERS 1988 TO 2 FEB 2005 (20050202/ED)

FILE BIOTECHDS
FILE LAST UPDATED: 1 FEB 2005 <20050201/UP>

>>> USE OF THIS FILE IS LIMITED TO BIOTECH SUBSCRIBERS <<<

>>> NEW CLASSIFICATION SYSTEM FROM 2002 ONWARDS - SEE HELP CLA <<<

>>> NEW DISPLAY FIELDS LS AND LS2 (LEGAL STATUS DATA FROM THE INPADOC DATABASE) AVAILABLE - SEE NEWS <<<

FILE CABA
FILE COVERS 1973 TO 7 Jan 2005 (20050107/ED)

This file contains CAS Registry Numbers for easy and accurate
substance identification.

The CABA file was reloaded 7 December 2003. Enter HELP RLOAD for details.

FILE WPIDS
FILE LAST UPDATED: 28 JAN 2005 <20050128/UP>
MOST RECENT DERWENT UPDATE: 200507 <200507/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

>>> FOR A COPY OF THE DERWENT WORLD PATENTS INDEX STN USER GUIDE,
PLEASE VISIT:
http://www.stn-international.de/training_center/patents/stn_guide.pdf <<<

>>> FOR DETAILS OF THE PATENTS COVERED IN CURRENT UPDATES, SEE
http://thomsonderwent.com/coverage/latestupdates/ <<<

>>> FOR INFORMATION ON ALL DERWENT WORLD PATENTS INDEX USER
GUIDES, PLEASE VISIT:
http://thomsonderwent.com/support/userguides/ <<<

>>> NEW! FAST-ALERTING ACCESS TO NEWLY-PUBLISHED PATENT
DOCUMENTATION NOW AVAILABLE IN DERWENT WORLD PATENTS INDEX
FIRST VIEW - FILE WPIFV.
FOR FURTHER DETAILS: http://www.thomsonderwent.com/dwpifv <<<

>>> NEW DISPLAY FORMAT HITSTR ADDED ALLOWING DISPLAY OF
HIT STRUCTURES WITHIN THE BIBLIOGRAPHIC DOCUMENT <<<

>>> SMILES and ISOSMILES strings are no longer available as
Derwent Chemistry Resource display fields <<<

>>> THE CPI AND EPI MANUAL CODES HAVE BEEN REVISED FROM UPDATE 200501.
PLEASE CHECK:
http://thomsonderwent.com/support/dwpiref/reftools/classification/code-rev
FOR DETAILS. <<<

FILE DRUGU
FILE LAST UPDATED: 2 FEB 2005 <20050202/UP>
>>> DERWENT DRUG FILE (SUBSCRIBER) <<<

>>> FILE COVERS 1983 TO DATE <<<
>>> THESAURUS AVAILABLE IN /CT <<<

Sensitivity of **two-stage PCR amplification** for detection of mycobacterium tuberculosis in paraffin-embedded tissues.

AUTHOR: Durmaz R.; Aydin A.; Durmaz B.; Aydin N.E.; Akbasak B.S.; Gunal S.

CORPORATE SOURCE: R. Durmaz, Department of Clinical Microbiology, Faculty of Medicine, Inonu University, Malatya, Turkey

SOURCE: Journal of Microbiological Methods, (1997) 29/2 (69-75). Refs: 29
ISSN: 0167-7012 CODEN: JMIMDQ

PUBLISHER IDENT.: S 0167-7012(97)00022-5

COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article

FILE SEGMENT: 004 Microbiology
005 General Pathology and Pathological Anatomy

LANGUAGE: English

SUMMARY LANGUAGE: English

AB In order to improve the sensitivity of polymerase chain reaction (PCR) for the detection of mycobacterial DNA in paraffin-embedded tissues, a new approach with two sets of specific primers in **two-stage PCR** was employed in specimens obtained from tuberculosis patients and controls. Thirty-nine paraffin blocks selected from patients who had been diagnosed as having tuberculosis by radiological evaluations, histopathological findings, and clinical symptoms and signs including response to antituberculous treatment were examined. The control group consisted of 10 specimens from individuals thai were proved to be negative for tuberculosis. After deparaffinization, lysis, phenol-chloroform extraction, and ethanol precipitation, the isolated DNA was amplified by PCR. Initially, all specimens were examined by the one- stage PCR using specific printers for 123-base pair (bp) fragment in IS6110 of mycobacterial DNA which yielded positive results only in 3 out of 39 (7.7%). In the **two-stage PCR** technique, 245 bp fragment of mycobacterial DNA was **amplified** at the first-step, then the PCR products were reamplified using the second specific **primer pairs** for 123-bp fragment. The true positivity of the **two-stage PCR** was 84.6% (33/39). The results indicate that **two-stage PCR** is more sensitive than one-stage (84.6% vs. 7.7%). All control specimens were negative by both PCR amplification methods, indicating that specificity of both methods was high. When the **two-stage amplification** was used, **PCR** positivity in the specimens obtained from different tissues was as follows: peritoneal and omental biopsies, 4/4; bone biopsies, 3/3; lymph node biopsies, 12/14; genito-urinary biopsies, 7/9; skin biopsies, 4/6; and one from each lung, breast, and pleural biopsies. PCR showed a good correlation with the granulomatous tissue reaction resulting in a 83.8% (31/37) positivity. The results indicate that the **two stage PCR amplification** can be used for detection of M. tuberculosis in paraffin-embedded tissues and is a useful technique in confirming tuberculosis in patients with clinically suspected disease who have acid-fast stain-negative.

Homogeneous multiplex genotyping of hemochromatosis mutations with fluorescent hybridization probes

AUTHOR(S): Bernard, Philip S.; Ajioka, Richard S.; Kushner, James P.; Wittwer, Carl T.
CORPORATE SOURCE: Departments of Pathology, University of Utah Medical School, Salt Lake City, UT, 84132, USA

SOURCE: American Journal of Pathology (1998), 153(4), 1055-1061
CODEN: AJPAA4; ISSN: 0002-9440
PUBLISHER: American Society for Investigative Pathology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Multiplex polymerase chain reaction amplification and genotyping by fluorescent probe melting temperature (**Tm**) was used to simultaneously detect multiple variants in the hereditary hemochromatosis gene. Homogenous real-time anal. by fluorescent melting curves has previously been used to genotype single base mismatches; however, the current method introduces a new probe design for fluorescence resonance energy transfer and demonstrates allele multiplexing by **Tm** for the first time. The new probe design uses a 3'-fluorescein-labeled probe and a 5'-Cy5-labeled probe that are in fluorescence energy transfer when hybridized to the same strand internal to an unlabeled **primer set**. Two hundred and fifty samples were genotyped for the C282Y and H63D hemochromatosis causing mutations by fluorescent melting curves. Multiplexing was performed by including two **primer sets** and two probe sets in a single tube. In clin. defined groups of 117 patients and 56 controls, the C282Y mutation was found in 87% (204/234) of patient chromosomes, and the relative penetrance of the H63D mutation was 2.4% of the homozygous C282Y mutation. Results were confirmed by restriction enzyme digestion and agarose gel electrophoresis. In addition, the probe covering the H63D mutation unexpectedly identified the A193T polymorphism in some samples. This method is amenable to multiplexing and has promise for scanning unknown mutations.

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=>

15 OF 21 BIOTECHDS COPYRIGHT 2005 THE THOMSON CORP. on STN
ACCESSION NUMBER: 2002-16045 BIOTECHDS
TITLE: Parallel sequencing of DNA, useful e.g. for detecting point mutations, by nested **polymerase chain reaction**, using outer primers in solution and immobilized internal primers;
DNA sequencing, **polymerase chain reaction** and DNA array for diagnosis and genomics
AUTHOR: ZELTZ P; SCHNEIDER S
PATENT ASSIGNEE: BIOCHIP TECHNOLOGIES GMBH
PATENT INFO: EP 1186669 13 Mar 2002
APPLICATION INFO: EP 2000-119182 5 Sep 2000
PRIORITY INFO: EP 2000-119182 5 Sep 2000
DOCUMENT TYPE: Patent
LANGUAGE: German
OTHER SOURCE: WPI: 2002-407210 [44]
AN 2002-16045 BIOTECHDS
AB DERWENT ABSTRACT:

NOVELTY - Specific determination of DNA sequences (I), comprising parallel amplification in a combined liquid/solid phase microarray system, using nested **polymerase chain reaction (PCR)**, with x **primer sets** (x = number of (I) being determined), each of at least three primers, is new.

DETAILED DESCRIPTION - Specific determination of DNA sequences (I), comprising parallel amplification in a combined liquid/solid phase microarray system, using nested **polymerase chain reaction (PCR)**, with x **primer sets** (x = number of (I) being determined), each of at least three primers, is new. Each **primer set** comprises: (a) two outer primers (P1, P2) that hybridize upstream and downstream of the target DNA (A) being amplified; and (b) an internal primer (P3) that hybridizes to (A) and can form an extension product (EP). The outer primers are present in the liquid phase, at an excess relative to P3, and P3 are irreversibly bound to a solid phase, forming a microarray of x spaced apart and defined positions. Determination is based on detecting an EP from P3 at defined array positions. INDEPENDENT CLAIMS are also included for the following: (1) determining point mutations by the novel method; (2) determining the sequence of (unknown) partial sequences of DNA by the new method; and (3) solid phase DNA array of P3.

BIOTECHNOLOGY - Preferred Process: In (1), all x variants to be detected are amplified using P3x primer families in which each member has, at its 3'-end, a different nucleotide (nt). The annealing temperature is chosen so that an EP will be formed only at the position on the array where the primer is exactly complementary to the position being analyzed. In (2), the method is similar but each member of the P3x primer family differs from all others by 1 to n nt at the 3'-end (n = length of the sequence being determined), and annealing conditions are as in (1). When the partial sequence being determined is unknown, all n nt are identified and the set of P3 comprises all possible permutations. Many P3 will hybridize to different regions and generate EP. EP are determined, correlated with array positions and their sequences combined (exploiting overlap regions) to assemble a complete sequence. In all cases, the polymerase used lacks 3'-5'-exonuclease activity. The outer primers are used in 10 to the power 2-10 to the power 12, especially 10 to the power 4, times excess over P3 and have a different **melting temperature** from P3. Preferred Array: The solid support has a surface of metal (e.g. aluminum or gold); metal/semimetal oxide; glass or polymer. Where the surface is metal/semimetal oxide or glass, primers are attached through a bifunctional silane that has 1-3 hydrolyzable groups attached to silicon, e.g. halo, 1-4C alkoxy or acyloxy or amino. The silane may include a second functional group that can undergo e.g. a nucleophilic substitution or addition reaction. The array may include some or all of the other reagents required for the process, e.g.

polymerase, buffer etc., and the external primers are reversible dehydrated on to the surface. Particularly it is formulated as a 'laboratory on a chip', with additional systems, for heating. cooling etc. integrated into the array.

USE - The method is used to determine point mutations, to sequence (unknown) regions of DNA, e.g. in genomics or proteomics analysis, and for diagnostic determination of analytes.

ADVANTAGE - The method is an economical, simple and error-free way for amplifying an array of DNA sequences without compromising sensitivity or specificity. Unlike known nested **PCR** in the liquid phase, dilution and re-establishment of a reaction mixture after the first reaction are not required, i.e. the total analysis needs only one working operation. The use of high annealing temperatures minimizes non-specific binding, making it possible to measure increases in mass at specific locations by physical methods, e.g. from changes in refractive index.

EXAMPLE - No relevant examples are given.(21 pages)

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